

SEQ ID No.	Source Organism	Element Name	Sequence
1	wheat	Em1a	TGCCGGACACGTGGCGCGA
2*	maize	ABRE1	TTCGAGAAGAACCGAGACGTGGCGGGC
3	maize	ABRE A	GCGCTCGCGCCACGTGGGATGCCGCC
4	maize	Prolamin P-box	GGTTGTCACATGTGAAAGGTGAAG
5	maize	Z2 and Z3 box	GATCATGCATGTCAATTCCACGTAGATAA
6	CaMV	35S AS-2	GTGGATTGATGTGATATCTC
7*	CaMV	35S AS-1 (As-1)	TCCACTGACGTAAGGGATGACGCACAAT
8	<i>Agrobacterium T-DNA</i>	OCS ele	TGACGTAAGCGCTTACGTCA
9	tobacco	GCC-box	GACTAATGGCGGCTTATCTCAC
10	soybean	GH3 D1	GCCCTCGTGTCTCCTCAATAAGCTA
11	soybean	GH3 D3	GCAATCCTTGTCCTCAATAAGTTCCAC
12	soybean	P3	AAGGGAGACAACTTGTCCTCCA
13	pea	GT-1 rbcS3A	ATCTTGTGGTTAATATGGCTGC
14	Arabidopsis	TCA motif	CTTCATCTCTCCTCCACCAAACG
15	Arabidopsis	C-repeat/DRE	ATTTCATGGCCGACCTGCTTTT
16	soybean	HSE	AGAAGCTTCCAGAAGCTCTAGAAG
17	maize	ERE	ATGCACGAATTGACCATTCC
18	parsley	gln2 PR box	CATAAGAGCCGCACTAAAATAAGACCG
19	wheat	HBP-1a	GGCCACGTCACCAATCCGCG
20	maize	A1 PROMOTER	CGGGTCAGTGTACCTACCAACCTAACAC
21	maize	Bz1 PROMOTER	CGTCTAACTGCGACTGGCAGGTGCGCAC
22	parsley	CHS promoter	ATCCGGTGGCCGTCCTCCACCTAACCT
23	rice tungro bacilliform virus	BoxII	CCAGTGTGCCCTGG
24*	rice	phyA GT-2 (GT-2)	TAGGTTAATTATTGGCGGTAAATTA
25	synthetic	GT-2 like	AAACGGTAAAAAGCGGTAGATTACC
26	oat	Phy PF1	GAAATAGCAAATGTTAAAATA
27	soybean	AT-com	AAAATAATTTAATATTATATTGAAA
28	Arabidopsis	AG site	ATAAGCTTACCATTAATGGTAAAGCTTGG
29	Arabidopsis	AP3 site	CAATACTTCCATTAGTAGTAAGCTT
30	Arabidopsis	TGAC motif	GGTATCGTTGACCGAGTTGACT
31	petunia	CAGT motif	TTGACAGTGTCACTTGACAGTGTAC
32	maize	Dof1/Dof2	GATCAAAAAGTGAGATC
33	parsley	pr2 oligomer II	ATTCAATAGTGTGCTAATTGTTAAGAGTTG
34	barley	CE1	TGCCATTGCCACCGGCCCCCA
35	soybean	H-box1	AGCAGACATGGTAGGCAGTGCA
36	bean	H-box2	TCACCTACCCCTACTCCCTATCC
37	barley	lox1	AATCGTCATGAATGAAGTCATGTGACGGCT
38	tobacco	PR-2d	AGGGGCAGCTCGACCTCCTCTCC
39	synthetic	ROL6	TCAGAACACGCAAGTGCAGCTACCCAAC
40	maize	SGB box 2/3	AGATATGCATGATCTTAAAC
41	maize	SGB box 6-8	TGCGGTTCTTGGCACAAATGGCATGA
42	maize	MS-BS7 box1-3	AAATCTACCTCCAACCAACCCAGCTTGT
43	maize	MS-BS7 box22-24	ATCACACCAACTTATCACCTAGAAAAGCGA
44	soybean	AuxRE DR5	CCTTTGTCTCCCTTTGTCTC
45*	rice	PCNA IIA	CGAGGTGGGCCGTAGGTGGGCCGTAT
46	parsley	PAL1 Box E	TACCTTTTACCCCTCATGTCATC
47	pea	lmyb26	GTCGACAAAAGTTAGGTTAGCAGGC
48	barley	GARE	GGCCGATAACAAACTCCGCC
49	tomato	E8	TTTTATTCCCAACAAATAGAAAGTCTTG
50	tobacco	E1RE	GATTTGGTCAGAAAGTCAGTCC
51	wheat	CA	GTAGTGCACCAAAACACAACATACCAAATTA
52	rape	napA	GATCCCACATACACATACACG
53	sunflower	HaG3-A -75	CAGCTCAAATGGTGATCTCTCTGG
54	sunflower	HaG3-A -111	TATACAGATGTAGCATGTCT
55	maize	Prolamin box	TTGACGTGAAAGTAAATTACAAC
56	pea	TGAC-like	GACACGTAGAATGAGTCATCAC
57	maize	SP20+6	GTCCCTCTCCCGTCCCAGAGAAACCC
58	tobacco	MSA RT1	TGTCCCCCAACGGTCTTATT
59*	Arabidopsis	DRE rd29A1 (DRE 1)	ATATCATACCGACATCAGTT
60	Arabidopsis	DRE rd29A2	ATATACTACCGACATGAGTT
61	Arabidopsis	CGF-1	GATAAAGATTACTCAGATATAACAAACGTT
62	tobacco	Itp1 D1	TTCCCCCTAGCTAGATACTTCATT
63	pea	ENBP1	CGATTATTGAGATATAAAATTAG
64	tomato	MRE	CGAAAACATACCGCGCAAATT

Figure 1

2-D Pooling of Transcription Factor Binding Sites (8 X 8)

Pool # 9 10 11 12 13 14 15 16

1	Em1a	ABRE1	ABREa	P-box	Z2Z3	As-2	As-1	Ocs
2	GCC	GH3D1	GH3D3	P3	GT-1	TCA	C/DRE	HSE
3	ERE	PRbox	HBP-1a	A1	Bz1	CHS	BoxII	GT-2
4	ROL	PF1	AT-com	AG	AP3	TGAC	CAGT	DOF
5	PR2	CE1	H-box1	H-box2	Lox1	PR-2d	ROL6	USA
6	USB	USC	USD	DR5	PCF	PAL1	myb26	GARE
7	E8	E1RE	CA	napA	HaG3.75	HaG3.111	P-box2	TGAC2
8	SP20+6	MSA	DRE1	DRE2	CCF1	Itp1D1	ENBP1	MRE

FIGURE 2



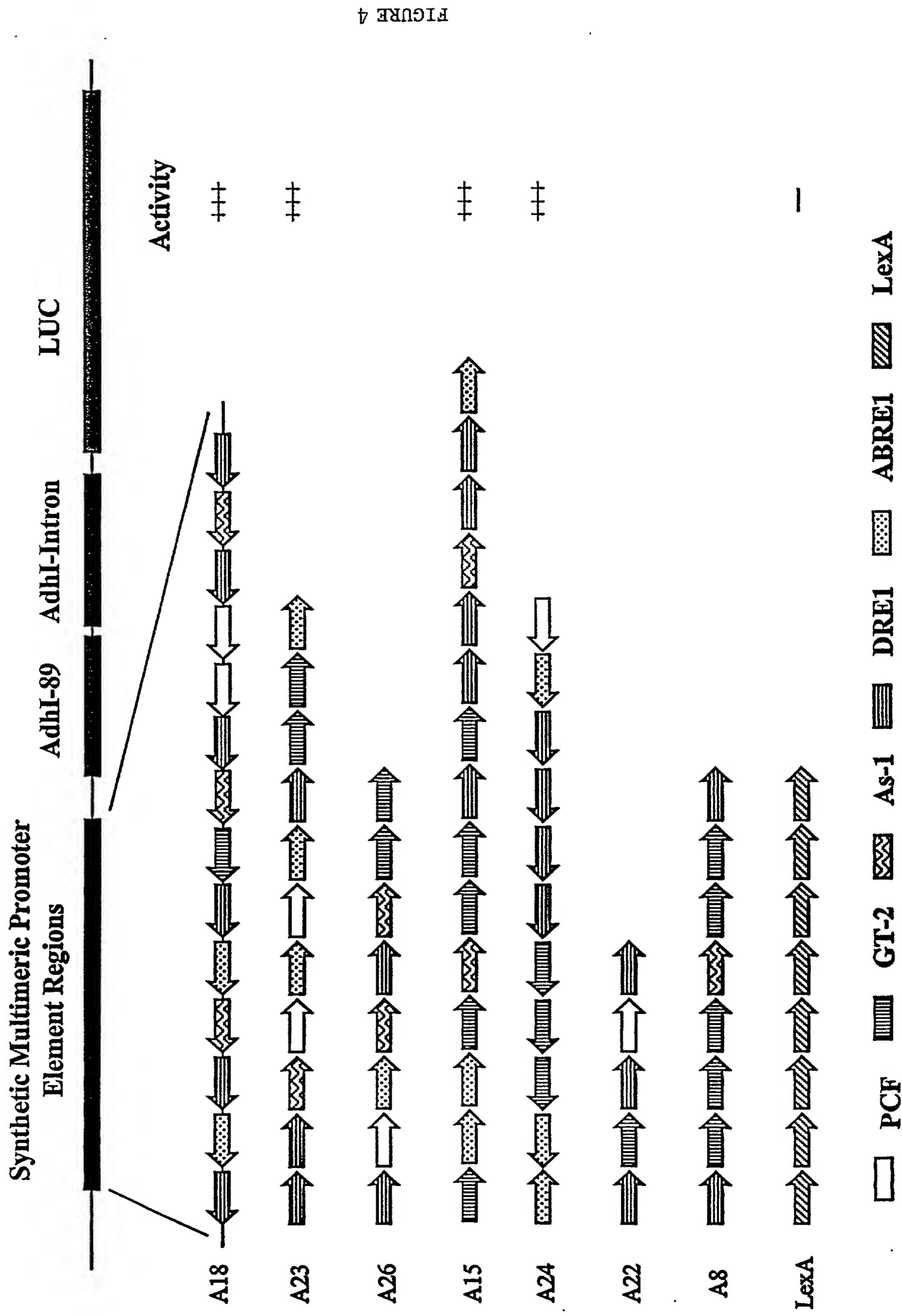
Strong Binding Activities in Maize Nuclear Extracts

	9	10	11	12	13	14	15	16
1	Em1a	ABRE1	ABREa	P-box	Z223	As-2	As-1	Ocs
2	GCC	GH3D1	GH3D3	P3	GT-1	TCA	C/DRE	HSE
3	ERE	PRbox	HBP-1a	A1	Bz1	CHS	BoxI	GT-2
4	ROL	PF1	AT-com	AG	AP3	TGAC	CAGT	DOF
5	PR2	CE1	H-box1	H-box2	Lox1	PR-2d	ROL6	USA
6	USB	USC	USD	DR5	PGF	PAL1	myb26	GARE
7	E8	E1RE	CA	napA	HAG3.75	HAG3.111	P-box2	TGAC2
8	SP20+6	MSA	DRE1	DRE2	CGF1	Itp1D1	ENBP1	MRE

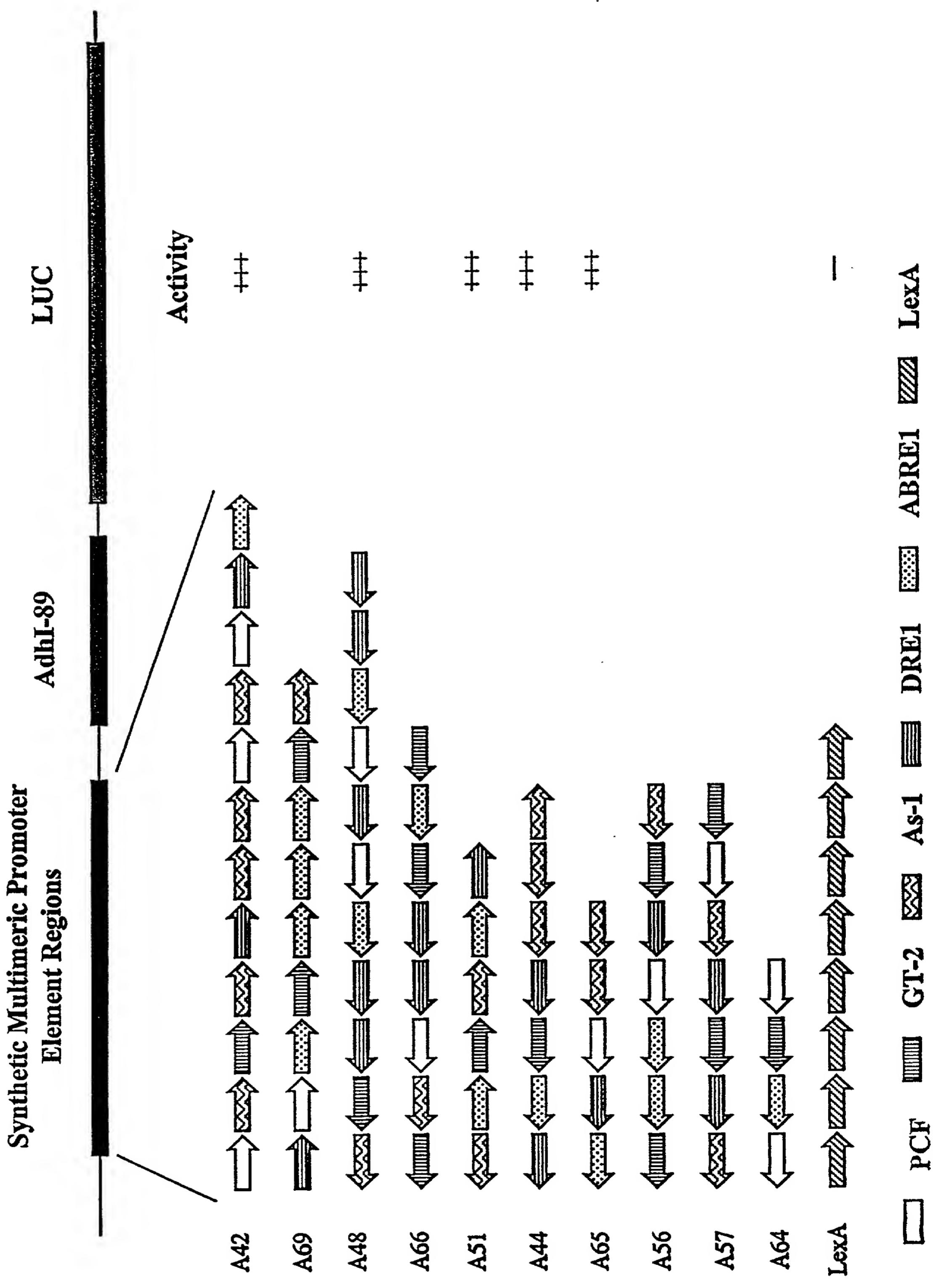
FIGURE 3

Transient Assay for Multimers of Transcription Factor Binding Sites

H H B P C F G T - 2 A s - 1 D R E 1 A B R E 1 LexA



Transient Assay for Multimers of Transcription Factor Binding Sites



Adh Intron Plus Constructs (root)

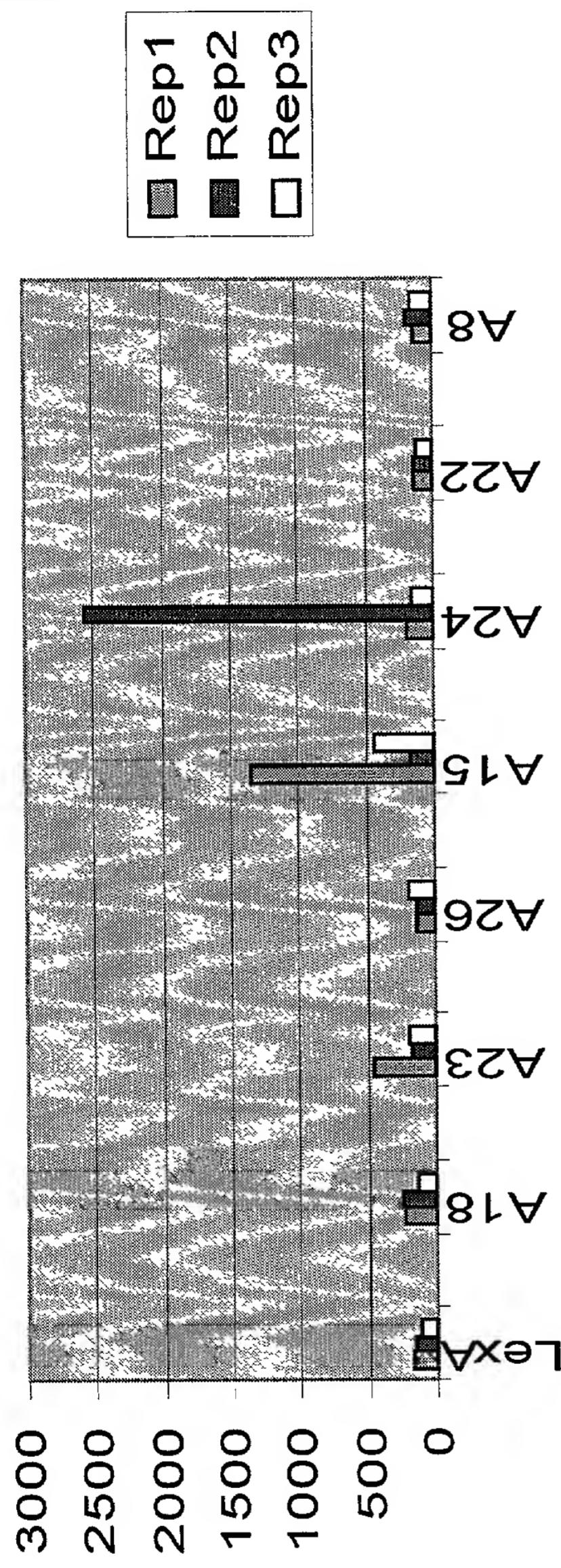


Figure 6a

Adh Intron Plus Constructs (shoot)

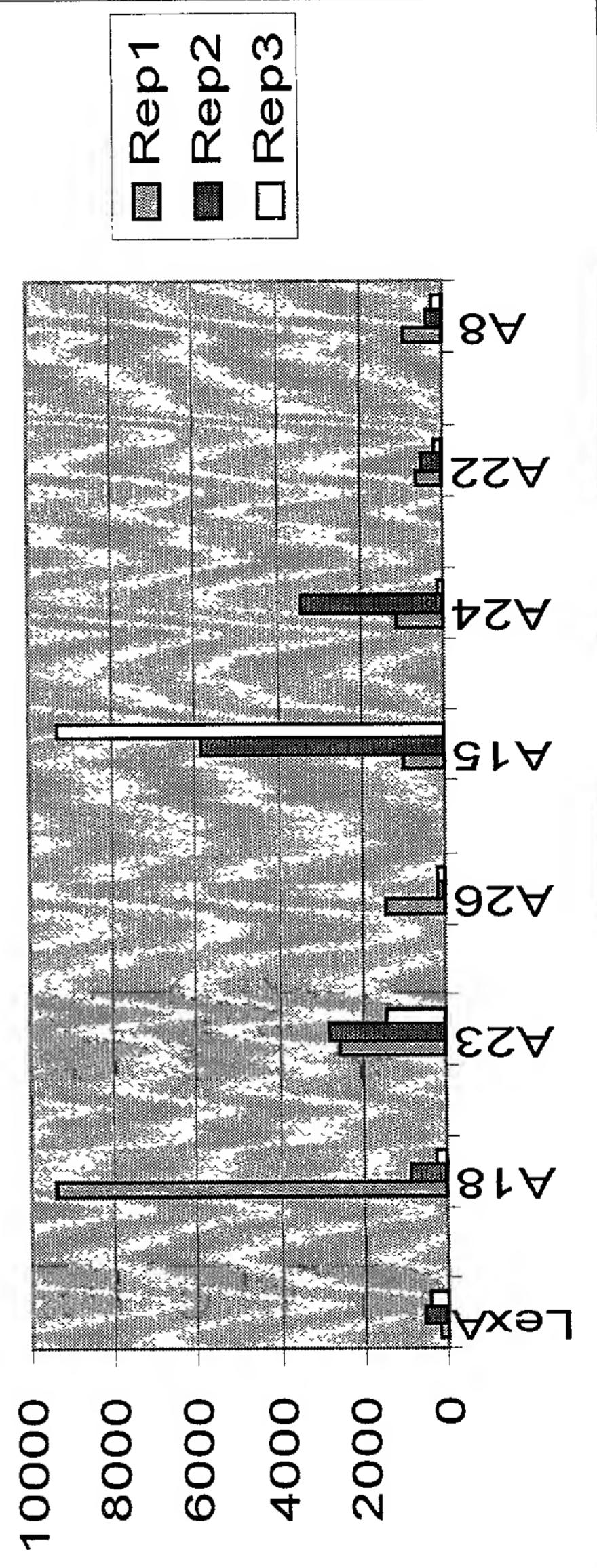


Figure 6b

Adh Intron Minus Constructs (root)

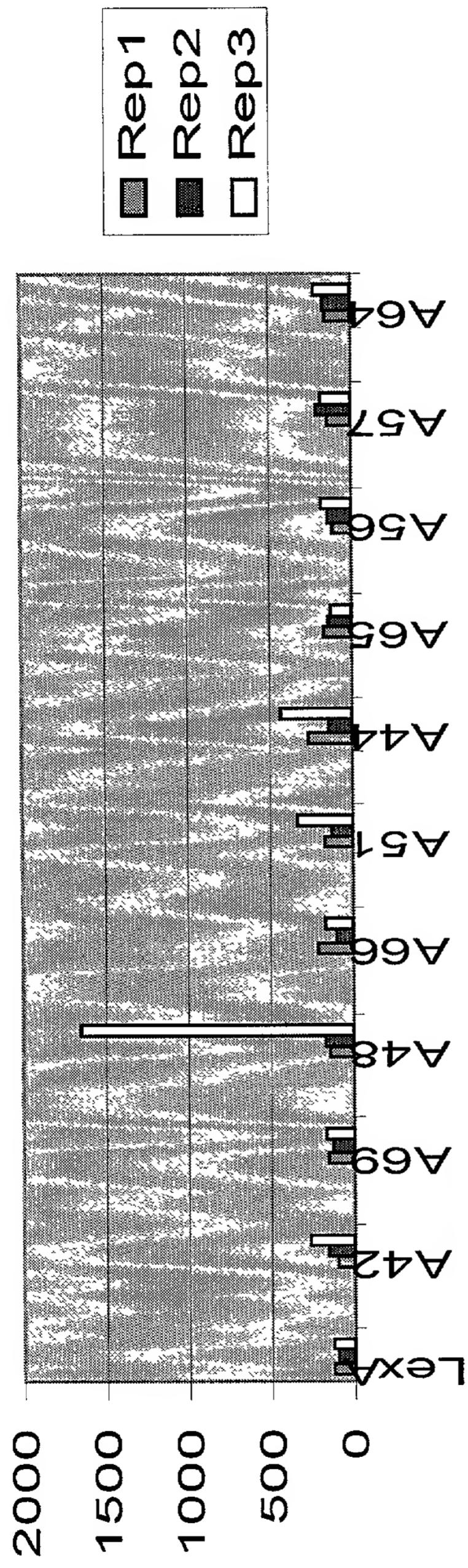


Figure 6c

Adh Intron Minus Constructs (shoot)

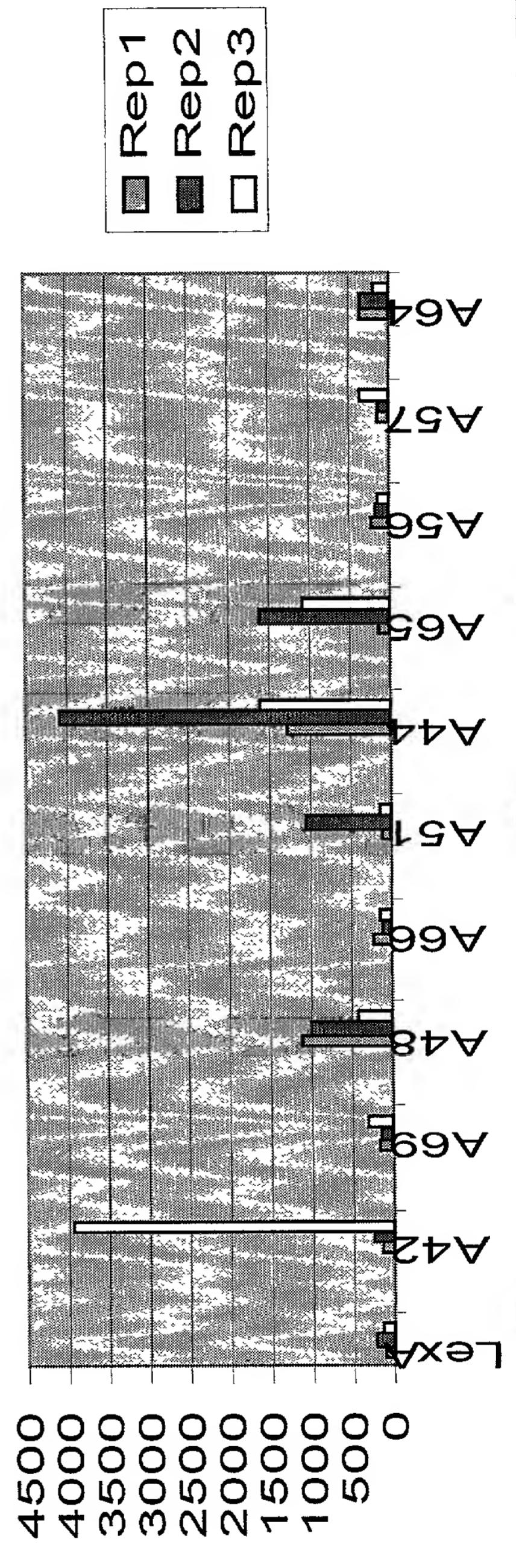


Figure 6d

A15 (PHP14147) 413bp

GT-2 ABRE1
TAGGTTAATTATTGGCGGTAATTAGCTCGAGAAGAACCGAGACGTGGCGGGCTAG
ABRE1 GT-2
CTTCGAGAAGAACGAGACGTGGCGGGCTAGCTAGGTTAATTATTGGCGGGTAATTATAG
AS-1 GT-2
CTCCACTGACGTAAGGGATGACGCACAATTAGCTAGGTTAATTATTGGCGATAATTATAG
GT-2 DRE1
CTAGGTTAATTATTGGCGGTAATTATAGCATATCATACCGACATCAGTTAGCTAGGTTA
GT-2 DRE1 DRE1
ATTATTGGCGGTAATTATAGCATATCATACCGACATCAGTTAGCATATCATACCGACAT
AS-1 DRE1
CAGTTTAGCTCCACTGACGTAAGGGATGACGCACAATTAGCATATCATACCGACATCAGT
DRE1 ABRE1
TTAGCATATCATACCGACATCAGTTAGCTCGAGAAGAACCGAGACGTGGCG

FIGURE 7

A18 (PHP14148) 392bp

DRE1 ABRE1
GCTAAACTGATGTCGGTATGATATGCTAGCCGCCACGTCTCGTTCTCGAAGCTAAACTGA
DRE1 AS-1 ABRE1
TGTCGGTATGATATGCTAATTGTGCGTCATCCCTTACGTCAGAGCTAGCCGCCACGTCTCG
DRE1 GT-2
GTTCTTCTCGAAGCTAAACTGATGTCGGTATGATATGCTATAATTACCGCCAATAATTACCTAG
AS-1 DRE1
CTAATTGTGCGTCATCCCTTACGTCAGAGCTAAACTGATGTCGGTAGATATGCTAATACGGGG
PCF PCF
CCCACCTACGGGCCACCTCGGCTAATACGGGCCACCTACGGGCCACCTCGGCTAAACTGATG
DRE1 AS-1 DRE1
TCGGTATGATATGCTAATTGTGCGTCATCCCTTACGTCAGAGCTAAACTGATGTCGGTATGA
TA

FIGURE 8

A23 (PHP14149) 314bp

DRE1 DRE1 AS - 1
TAGCATATCATACCGACATCAGTTAGCATATCATACCGACATCAGTTAGCTCCACTGACGTAA
PCF1 ABRE1
GGGATGACGCACAATTAGCCGAGGTGGGCCGTAGGTGGGCCGTATTAGCTTCGAGAAGAACCG
PCF1 ABRE1
AGACGTGGCGGGCTAGCCGAGGTGGGCCGTAGGTGGGCCGTATTAGCTTCGAGAAGAACGTGAG
DRE1 GT - 2
ACGTGGCGGGCTAGCATATCATACCGACATCAGTTAGCTAGGTTAATTATTGGCGGTAAATTATA
GT - 2 ABRE1
GCTAGGTTAATTATTGGCGGTAAATTATAGCTTCGAGAAGAACCGAGGACGTGGC

FIGURE 9

A24 (PHP14150) 278bp

ABRE1 ABRE1 GT-2
TAGCTTCGAGAAGACGTGGCGGCCACGTCTCGTTCTCGAAGCTATAATTACCGCCAA
GT-2 GT-2
TAATTAACCTAGCTATAATTACCGCCAATAATTACCTAGCTATAATTACCGCCAATAATTAAACC
DRE1 DRE1 DRE1
TAGCTAAACTGATGTCGGTATGATATGCTAAACTGATGTCGGTATGATATGCTAAACTGATGTCG
DRE1 ABRE1
GTATGATATGCTAAACTGATGTCGGTATGATATGCTAGCCCCACGTCTCGTTCTCGAAG
PCF
CTAATACGGGCCACCTA

FIGURE 10

A42 (PHP14151) 348bp

PCF AS -1
CGAGGTGGGCCGTAGGTGGGCCGTATTAGCTCCACTGACGTAAGGGATGACGCACAATTAGCT
GT -2 AS -1
AGGTAAATTATTGGCGGTAATTATAGCTCCACTGACGTAAGGGATGACGCACAATTAGCATATCA
DRE1 AS -1 AS -1
TACCGACATCAGTTAGCTCCACTGACGTAAGGGATGACGCACAATTAGCTCCACTGACGTAAGG
PCF AS -1
GATGACGCACAATTAGCCGAGGTGGGCCCGAGGTGGGCCGTATTAGCATATCATACCGACATCAGTTA
ABRE1 DRE1
GCTTCGAGAAGAACCGAGTCGAG

FIGURE 11

A44 (PHP14152) 198bp

DRE1

ABRE1

TAAACTGATGTCGGTATGATAATGCCAACCCGGCACGTCCC GGTTCTCTCGAAGCTATAATT
GT-2 DRE1 ABRE1
CCGCCAATAATTAACCTAGCTAAACTGATGTCGGTATGATATGCTAATTGTGCGTCATCCCTTAC
As-1 As-1 As-1
GTCAGTGGAGCTAATTGTGCGTCATCCCTTACGTCACTGGAGCTCCACTGAACGTAAGGGATGAC
GTC

FIGURE 12

A48 (PHP14153)

302bp

AS - 1

GT - 2

TTGTGCGTCATCCCTTACGTCAGGTGGAGTAATTACCGCCAATAATTAACCTAGCTAAACTGATGT
DRE1 DRE1 ABRE1
CGGTATGATATGCTAAACTGATGTCGGTATGATATGCTAGGCCCGCCACGTCTCGTTCTCGA
PCF DRE1
AGCTAATACGGGCCACCTACGGGCCACCTCGGGCTAAACTGATGTCGGTATGATATGCTAATAC
PCF ABRE1
GGGCCACCTACGGGCCACCTCGGGCTAGGCCCGCCACGTCTCGTTCTCGAAAGCTAAACTGA
DRE1 DRE1
TGTCGGTATGATATGCTAAACTGATGTCGGTATGATATGCTA

FIGURE 13

A51 (PHP14154) 157bp

AS -1 ABRE1
GTGCGTCATCCCTTACGTCAGTGGAGCTTCGAGAAGAACGAGACGTGGCGGCTAGCTAGGTTA
GT -2 AS -1 ABRE1
ATTATTGGCGGTAATTATAGCTCCACTGACGTAAGAGCTCGAGAAGAACGAGACGTGGCGGC
DRE1
TAGCATATCATACCGACATCAGTTAG

FIGURE 14